

QY 1 AAV6PQHPQPPRYGHCVTDSGVVYSGVMOLKTQGNOMLCTCLNGVSCQETAVTQT 6

QY 1 AAVYQPPHPPPPYGHCTDGSVYVSVGMOMLKTGKMKLCTCLGNGVSCQETAVTOT 60
DB 291 AAVYQPPHPPPPYGHCTDGSVYVSVGMOMLKTGKMKLCTCLGNGVSCQETAVTOT 350
QY 61 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGLHMCSTTSNVEDQKYSFCTDHTVLVOT 120
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGLHMCSTTSNVEDQKYSFCTDHTVLVOT 410
QY 121 RGSNSGALCHFPFLYNNHNTDCTSEGRDNMKKCTTONTADQKFGFCPMAAHEEIC 180
DB 411 OGSNSGALCHFPFLYNNHNTDCTSEGRDNMKKCTTONTADQKFGFCPMAAHEEIC 470
QY 181 TTNEGVMYRIGDQMDKQHDGMHMRCTCVNGRGEMTCIAVSOLRDCIYDDITVYVNDT 240
DB 471 TTNEGVMYRIGDQMDKQHDGMHMRCTCVNGRGEMTCIAVSOLRDCIYDDITVYVNDT 530
QY 241 FHKRHEEGHMLNCTCFQGRGRRKCDPVDCQDSEGTFTYQIGDSMEKYVHGVRQCYCY 300
DB 531 FHKRHEEGHMLNCTCFQGRGRRKCDPVDCQDSEGTFTYQIGDSMEKYVHGVRQCYCY 590
QY 301 GRGIGEMHCOPLOTYPSSSGPVYEVFTETPSQPNSHPIOW 340
DB 591 GRGIGEMHCOPLOTYPSSSGPVYEVFTETPSQPNSHPIOW 630

RESULT 2

US-08-551-356-2

Sequence 2, Application US/08551356

Patent No. 5830700

GENERAL INFORMATION:

APPLICANT: Iranl, Meher

TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 4225 Roosevelt Way, N.E.

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/551.356

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/349.762

FILING DATE:

APPLICATION NUMBER: US/07/998.271

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: HOLLY, Julie A

REGISTRATION NUMBER: 33-246

REFERENCE/DOCKET NUMBER: 92-26

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-547-8080 ext 322

TELEFAX: 206-548-2329

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2446 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-551-356-2

Query Match 99.58; Score 1978; DB 2; Length 2446;
Best Local Similarity 99.48; Pred. No. 3.3e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVYQPPHPPPPYGHCTDGSVYVSVGMOMLKTGKMKLCTCLGNGVSCQETAVTOT 60
DB 291 AAVYQPPHPPPPYGHCTDGSVYVSVGMOMLKTGKMKLCTCLGNGVSCQETAVTOT 350
QY 61 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGLHMCSTTSNVEDQKYSFCTDHTVLVOT 120
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGLHMCSTTSNVEDQKYSFCTDHTVLVOT 410
QY 121 RGSNSGALCHFPFLYNNHNTDCTSEGRDNMKKCTTONTADQKFGFCPMAAHEEIC 180
DB 411 OGSNSGALCHFPFLYNNHNTDCTSEGRDNMKKCTTONTADQKFGFCPMAAHEEIC 470
QY 181 TTNEGVMYRIGDQMDKQHDGMHMRCTCVNGRGEMTCIAVSOLRDCIYDDITVYVNDT 240
DB 471 TTNEGVMYRIGDQMDKQHDGMHMRCTCVNGRGEMTCIAVSOLRDCIYDDITVYVNDT 530
QY 241 FHKRHEEGHMLNCTCFQGRGRRKCDPVDCQDSEGTFTYQIGDSMEKYVHGVRQCYCY 300
DB 531 FHKRHEEGHMLNCTCFQGRGRRKCDPVDCQDSEGTFTYQIGDSMEKYVHGVRQCYCY 590
QY 301 GRGIGEMHCOPLOTYPSSSGPVYEVFTETPSQPNSHPIOW 340
DB 591 GRGIGEMHCOPLOTYPSSSGPVYEVFTETPSQPNSHPIOW 630

RESULT 3

PCT-US93-12687-2

Sequence 2, Application PC/TUS9312687

GENERAL INFORMATION:

APPLICANT: Iranl, Meher H.

TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 4225 Roosevelt Way, N.E.

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12687

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/998.271

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, Gary E

REGISTRATION NUMBER: 31-648

REFERENCE/DOCKET NUMBER: 92-26PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-547-8080 ext 322

TELEFAX: 206-548-2329

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2446 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-12687-2

Query Match 99.58; Score 1978; DB 4; Length 2446;
Best Local Similarity 99.48; Pred. No. 3.3e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVYQPPHPPPPYGHCTDGSVYVSVGMOMLKTGKMKLCTCLGNGVSCQETAVTOT 60
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OM protein - protein search, using SW model

Run on: October 4, 2000, 18:05:04 ; Search time 49.12 Seconds
(Without alignments) 163.951 Million cell updates/sec

Title: US-09-507-691-1_COPY_2_341

Perfect score: 1988
Sequence: 1 AAVYQPPHQPDPYCHCT.....PEVEFITETSPQNSHPIDW 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1979	99.5	2386 1	W63171 Amino acid sequence
2	1979	99.5	2477 1	W95595 Human fibronectin.
3	1978	99.5	2324 1	R92778 Human fibronectin.
4	1978	99.5	2327 1	P70373 Human fibronectin
5	1978	99.5	2446 1	R60021 Fibriogen-alpha.
6	1973	99.2	2327 1	R15468 Human fibronectin.
7	386	19.4	663 1	W41227 Chicken matrix met
8	382.5	19.2	631 1	P96143 Sequence of human
9	382.5	19.2	631 1	W41226 Human mature matrl
10	382.5	19.2	660 1	R06420 Type IV collagenas
11	382.5	19.2	663 1	W41111 Chicken matrix met
12	381.5	19.2	631 1	P91139 Human type IV coll
13	380	19.1	429 1	W41112 Human matrix metal
14	379	19.1	631 1	R07969 Complete type IV c
15	374	18.8	707 1	R07077 92-kDa human type
16	371	18.7	65 1	W62372 Antithrombotic pep
17	348	17.5	60 1	W62371 Antithrombotic pep
18	290	14.6	48 1	W62375 Antithrombotic pep
19	278	14.0	48 1	W62373 Antithrombotic pep
20	258	13.0	43 1	W62374 Antithrombotic pep
21	240	12.1	411 1	R11672 Cell adhesive and
22	239.5	12.0	420 1	R11666 Cell adhesive and
23	239.5	12.0	422 1	R11665 Cell adhesive and
24	237	11.9	409 1	R11675 Cell adhesive and
25	232	11.7	133 1	R12784 Fibrin-binding pol
26	232	11.7	134 1	R12783 Fibrin-binding pol
27	232	11.7	144 1	R12782 Fibrin-binding pol
28	232	11.7	145 1	R12781 Fibrin-binding pol
29	232	11.7	188 1	R42169 Hemopoietic stem
30	232	11.7	192 1	P91467 Peptide with fibrin
31	232	11.7	192 1	W01635 Functional fragmen
32	232	11.7	192 1	W44859 Human fibronectin
33	216.5	10.9	366 1	R11674 Cell adhesive and

34	215	10.8	377 1	R11668 Cell adhesive and
35	214	10.8	375 1	R11671 Cell adhesive and
36	206	10.4	37 1	W62370 Antithrombotic pep
37	195.5	9.8	1463 1	R63575 Group 1 phospholip
38	195.5	9.8	1463 1	R63575 Bovine phospholip
39	193.5	9.7	1479 1	W44119 Human type C lecti
40	193	9.7	1456 1	R24033 Soluble mannose re
41	187	9.4	1479 1	W44118 Murine type C lect
42	170	8.6	655 1	R89197 Human hepatocellul
43	163	8.2	655 1	R53962 Hepatocyte growth
44	143	7.2	1722 1	W38429 Human dendritic ce
45	137.5	6.9	1723 1	W06645 Mouse DEC-205. L19

ALIGNMENTS

RESULT 1	
ID W63171	W63171 standard; peptide: 2386 AA.
AC W63171	27-OCT-1998 (first entry)
DE Amino acid sequence of fibronectin.	
KW Mast cell protease; MCP: mouse; inhibitor; peptide substrate; asthma;	
KW Trypsin-6; protein; inflammatory disorder; allergic rhinitis; urticaria;	
KW Anticodema; eczematous dermatitis; atopic dermatitis; anaphylaxis;	
KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;	
KW Inflammatory skin condition; fibronectin.	
OS Mus sp.	
PN W09833812-A1.	
PD 06-AUG-1998.	
PF 30-JAN-1998; 001865.	
PR 05-FEB-1997; US-037090.	
PA (BCHM) BRIGHAM & WOMENS HOSPITAL.	
PI Huang C, Stevens RL;	
DR MPI: 98-437390/37.	
PT Trypsin-6 complex inhibitory peptides - used to treat mast	
PR cell-mediated inflammatory disorders e.g. asthma	
PS Disclosure: Pages 36-42; 69pp; English.	
CC This is the amino acid sequence of fibronectin. The trypsin-6 complex	
CC inhibitory peptides of the invention comprise the sequence of a fragment	
CC of the fibronectin (residues 1351-1356). Sequences shown in W63160 to	
CC W63169 represent mouse mast cell protease (MCP-6) inhibitory peptides.	
CC These peptides which are trypsin-6 complex inhibitors, can be used for	
CC treating a mast cell-mediated inflammatory disorder. The inhibitors can	
CC be used to treat inflammatory disorders including asthma, allergic	
CC rhinitis, urticaria and anticodema, eczematous dermatitis (atopic	
CC dermatitis), anaphylaxis, hyperproliferative skin disease, peptic ulcers,	
CC inflammatory bowel disorder, hyperresponsiveness and inflammatory skin	
CC conditions.	
SO Sequence 2386 AA:	

Query Match	99.5%; Score 1979; DB 1; Length 2386;
Best Local Similarity	99.4%; Pred. No. 1.3e-141;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY 1 AAVYQPPHQPDPYCHCTDSGVYVSGMQLKTQGNKMLCTGNGVSCQETAVYOT 60	
DB 291 AAVYQPPHQPDPYCHCTDSGVYVSGMQLKTQGNKMLCTGNGVSCQETAVYOT 350	
QY 61 YGNSNGEPCVLEPTTNGRTFYSCCTEERQDGLMCTSTNYSDOKYSFCTDHTVLVOT 120	
DB 351 YGNSNGEPCVLEPTTNGRTFYSCCTEERQDGLMCTSTNYSDOKYSFCTDHTVLVOT 410	
QY 121 RGNSNGALCHFFPLNNNNYTDCTSEGRBNMKWCTTONTYADOKRFGCMAHEITC 180	
DB 411 RGNSNGALCHFFPLNNNNYTDCTSEGRBNMKWCTTONTYADOKRFGCMAHEITC 470	
QY 181 TTNGSVYRIGDQMDKQHDGKHMNCCTGNGRBNMCIAVSOLRQCIYDITVNVDT 240	
DB 471 TTNGSVYRIGDQMDKQHDGKHMNCCTGNGRBNMCIAVSOLRQCIYDITVNVDT 530	

OM protein - protein search, using sw model

Run on: October 4, 2000, 18:01:21 ; Search time 44.67 Seconds
(without alignments)
127.576 Million cell updates/sec

Title: US-09-507-691-1_COPY_2_341

Sequence: 1 AAVQPPHPQPPYGHCVT.....PVEVFTETPSQPSHPIDM 340

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:*
3: /cgnl_7/ptodata/1/1aa/6_COMB.pep:*
4: /cgnl_7/ptodata/1/1aa/PCRTUS_COMB.pep:*
5: /cgnl_7/ptodata/1/1aa/Backlist.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	99.5	2386	2 US-09-016-366A-12	Sequence 12, Appl
2	1978	99.5	2446	2 US-08-551-356-2	Sequence 2, Appl
3	1978	99.5	2446	4 PCT-US93-12687-2	Sequence 2, Appl
4	1973	99.2	2327	5 5455158-1	Patent No. 5455158
5	1971	99.1	2324	1 US-08-283-857-1	Sequence 1, Appl
6	1971	99.1	2324	4 PCT-US95-09819-1	Sequence 16, Appl
7	1959	98.5	2231	1 US-08-153-799-16	Sequence 18, Appl
8	382.5	19.2	660	3 US-08-704-711A-18	Sequence 19, Appl
9	374	18.8	707	3 US-08-704-711A-19	Sequence 19, Appl
10	371	18.7	65	2 US-08-982-597A-19	Sequence 19, Appl
11	371	18.7	65	3 US-09-136-218-19	Sequence 19, Appl
12	348	17.5	60	2 US-08-982-597A-18	Sequence 18, Appl
13	348	17.5	60	3 US-09-136-218-18	Sequence 18, Appl
14	290	14.6	48	2 US-08-982-597A-22	Sequence 22, Appl
15	290	14.6	48	3 US-09-136-218-22	Sequence 22, Appl
16	278	14.0	48	2 US-08-982-597A-20	Sequence 20, Appl
17	278	14.0	48	3 US-09-136-218-20	Sequence 20, Appl
18	258	13.0	43	2 US-08-982-597A-21	Sequence 21, Appl
19	258	13.0	43	3 US-09-136-218-21	Sequence 21, Appl
20	243	12.2	474	2 US-08-836-854-9	Sequence 9, Appl
21	239.5	12.0	422	2 US-08-836-854-12	Sequence 12, Appl
22	232	11.7	188	1 US-08-142-449B-14	Sequence 14, Appl
23	206	10.4	37	2 US-08-982-597A-17	Sequence 17, Appl
24	206	10.4	37	3 US-09-136-218-17	Sequence 17, Appl
25	202	10.2	1455	3 US-08-840-062-5	Sequence 5, Appl
26	195.5	9.8	1463	1 US-08-840-062-5	Sequence 11, Appl
27	193.5	9.7	1479	3 US-08-840-062-4	Sequence 4, Appl
28	187	9.4	1479	3 US-08-840-062-2	Sequence 2, Appl

29	180.5	9.1	1487	3 US-08-840-062-7	Sequence 7, Appl
30	170	8.6	655	1 US-08-148-910-12	Sequence 12, Appl
31	170	8.6	655	1 US-08-448-937A-12	Sequence 12, Appl
32	140.5	7.1	1449	3 US-08-840-062-6	Sequence 6, Appl
33	130	6.5	24	2 US-08-982-597A-23	Sequence 23, Appl
34	130	6.5	24	3 US-09-136-218-23	Sequence 23, Appl
35	127.5	6.4	1833	3 US-08-479-722B-2	Sequence 2, Appl
36	127.5	6.4	1833	4 PCT-US95-02251-18	Sequence 18, Appl
37	123	6.2	96	2 US-08-717-169-2	Sequence 7, Appl
38	121.5	6.1	2214	1 US-08-727-034-7	Sequence 7, Appl
39	120.5	6.1	2213	1 US-08-727-034-3	Sequence 3, Appl
40	116.5	5.9	574	5 5378464-3	Patent No. 5378464
41	114.5	5.8	2556	1 US-08-185-432-17	Sequence 17, Appl
42	114.5	5.8	2556	1 US-08-083-590A-20	Sequence 20, Appl
43	114.5	5.8	2556	3 US-08-532-384-20	Sequence 20, Appl
44	114	5.7	810	2 US-08-820-170A-34	Sequence 34, Appl
45	114	5.7	810	3 US-09-055-699-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-016-366A-12
Sequence 12, Application US/09016366A
Patent No. 5455431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plummer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-366A-12

Query Match 99.5% Score 1979: DB 2: Length 2386:
Best Local Similarity 99.4% Pred. No. 2.6e-174:
Matches 338: Conservative 1: Mismatches 1: Indels 0: Gaps 0: